Figure 1

SSSVNVSSNL -

Sequence and pentamer URS distribution nterieukin-8 receptoi-Ar Seqidr ENSP00000295688

HSammern receptor Scold ENSP0000278028

Sequence and pentamer URS distribution

LYTVSISVADLEVGAVVMPMNGLYLIMSK IWSLGRIPLGIEWUSMDYVASTASIFSVETLOIDR YRI

SVQQPIR YIK YR IK TR ASATTUGAWFILSTIMVIPIIGMNHEMQQTSVR R EDK GET<u>DHYD</u>V

<u>IPPPUIDMENTAAK TYK AVRIOHCOHRUSISINK SIPSTSTIK UR PENPK G</u>

DAKIK PGKU<u>ESPMEVIKURUKURIKOPK DAGGGSWIKUSPSQTPK EMKUSPWWESQEDDRUEVDKUYC</u>

<u>fpldtvhwoaaaecssrudyvavnrushcolkudboclnthcaselsedomicdsosesrudsdtt</u>

TETAPGK GKILDRISGSNTGLDYTKIFTWKIRILDRISHSRIOYVSGLHMNRIJER KIZAKIQLGFIMA

<u> THE HOLD METERWATER OF NEGNERHMEDTATES TO STITUTE THE CHENEX OF THE STATES. TO STATE THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES. THE STATES OF THE STATES. THE STATES OF THE</u>

T) S

Figure 2

Figure 3

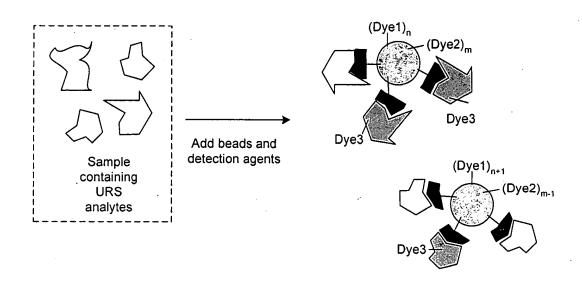


Figure 4

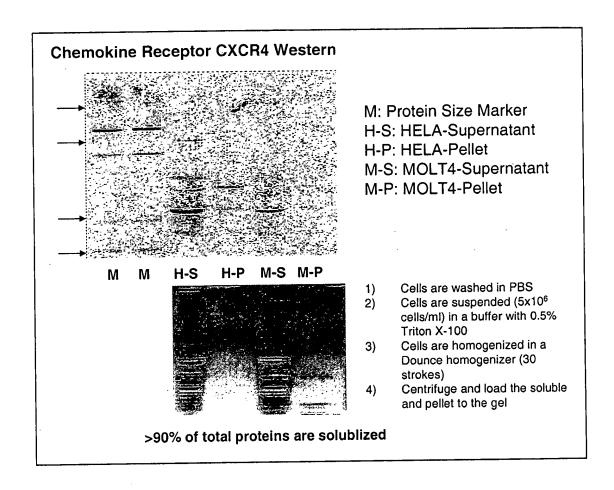


Figure 5

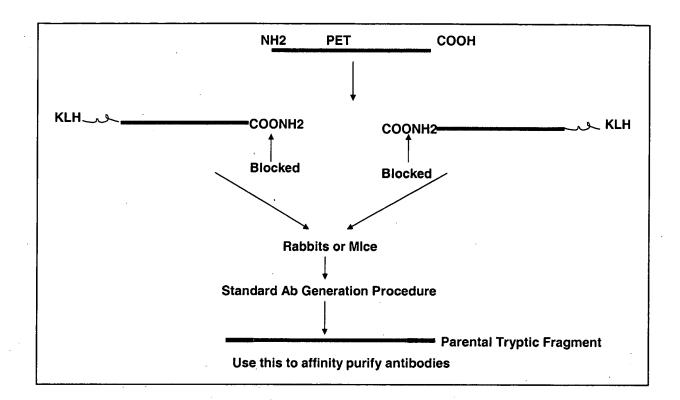


Figure 6

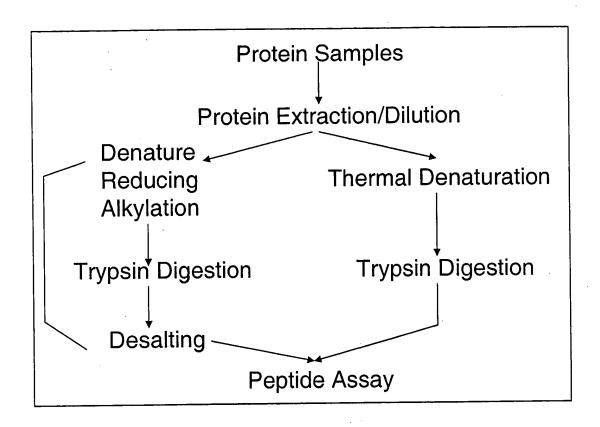


Figure 7

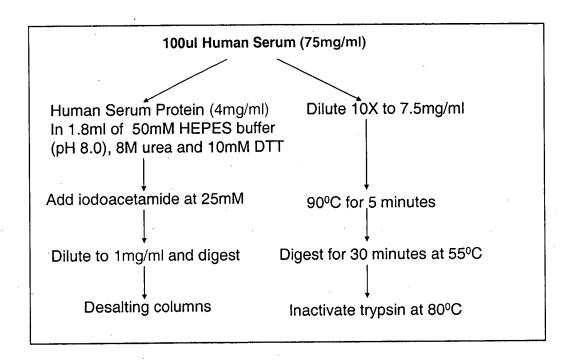


Figure 8

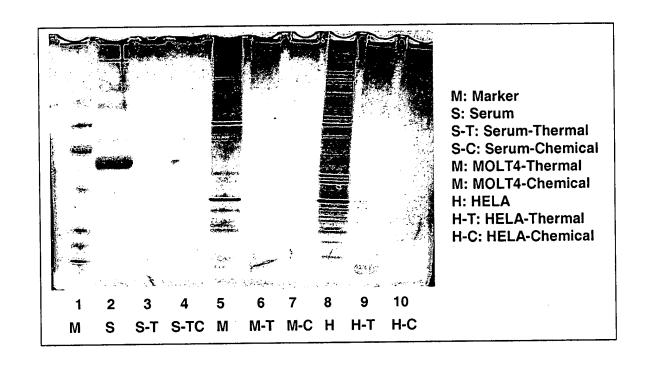


Figure 9

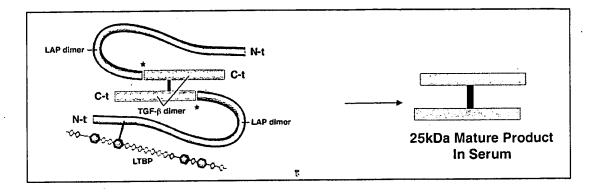


Figure 10

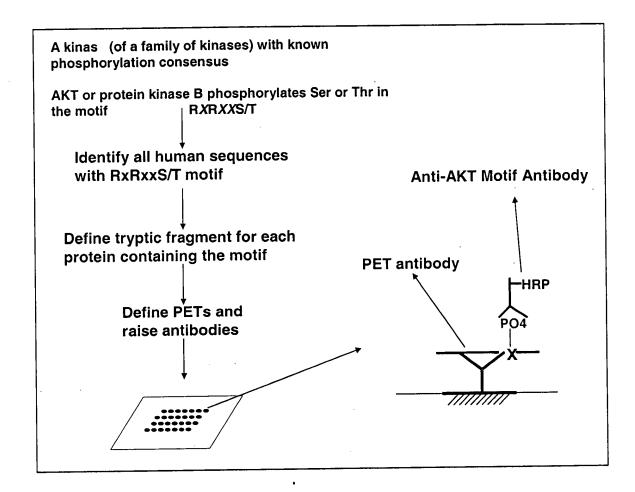


Figure 11

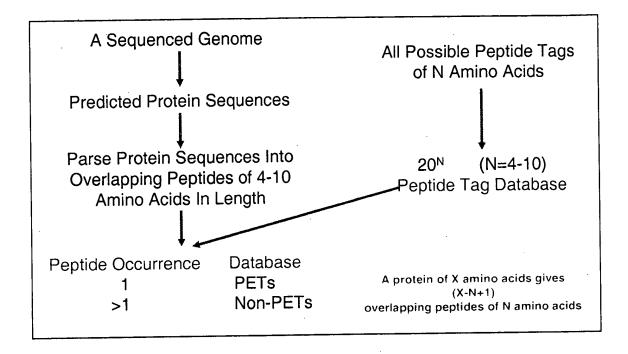


Figure 12

Tag Length (amino acids)	All Possible Tags	Total PETs	Total Non-PETs (non-redundant)
4 5 6 7 8 9 10	160,000 3.2×10 ⁶ 6.4×10 ⁷ 1.28×10 ⁹ 2.56×10 ¹⁰ 5.12×10 ¹¹ 1.02×10 ¹³	745 560,309 4,609,172 6,652,224 7,018,340 7,138,933 7,216,090	158,862 1,684,684 2,350,532 1,848,908 1,744,029 1,714,971 1,695,512
29,076 human pro ~12M overlapping	tein sequences analyzed 4-10mr peptides	% of Human Peptide Tags in Total Tag Space in Total Tag Space	Dapase found in Human Proteome

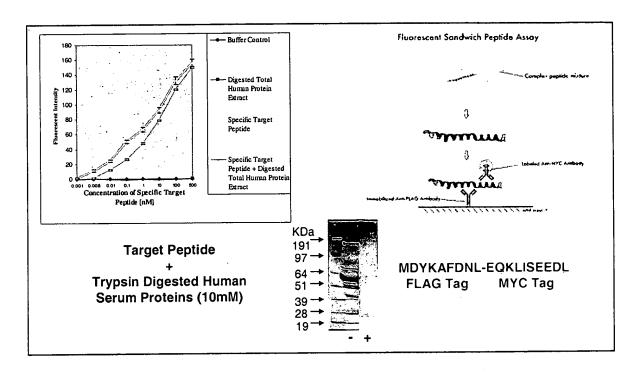
Figure 13

in of PET (a	mino acids)	Prot ins with PETs	Proteome Coverage
4		684	2.35%
5		23,446	80.64%
6		26,069	89.66%
7		26,184	90.05%
8		26,216	90.16%
9		26,238	90.24%
10		26,250	90.28%
Average PET per Tagged Protein	250- 200- 150- 100- 50- 0 4 5	6 7 8 9 10	
	PET L	ength (amino acids)	

Figure 14

PET Length (Amino Acids)	_	s/Tagged Protein Trypsin Cleavage
5 6	24 177	16 98
8	268	129
700 600 500 400 300 100	200000 150000 100000 50000 100000	X= ~8.5
1 21 41 61 81 101 12 Fragment Num		1 11 21 31 41 51 61 71 81 91 Fragment Size (amino acids)

Figure 15



BEST AVAILABLE COPY

JUST AVAILABLE COPY

Figure 16

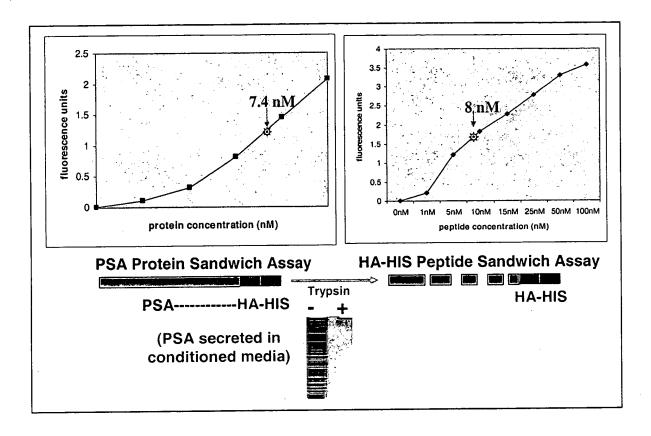


Figure 17

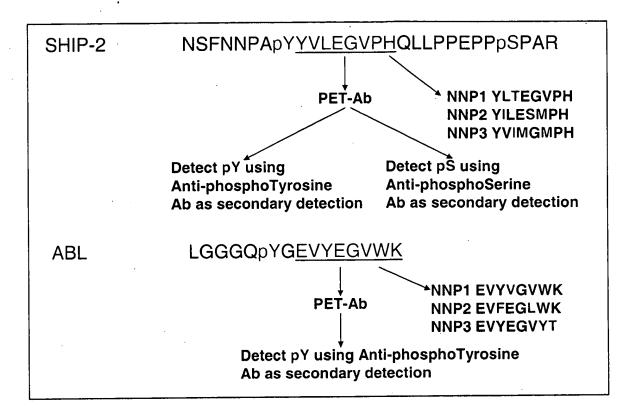


Figure 18

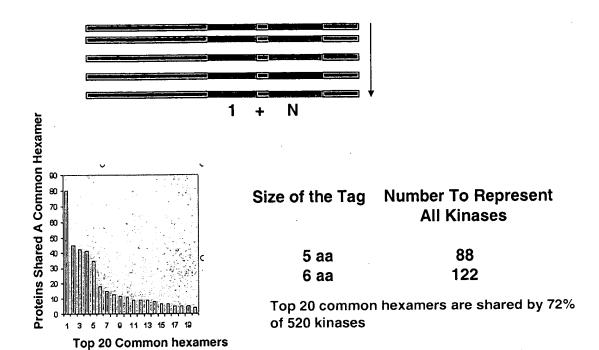


Figure 19

Protein	Parental Tryptic Peptide	Also Detect
BRAF	WSGSHQFEQLSGSILWMAPEVIR*	
DLK	MSFAGTVAWMAPEVIR	
GCK	SFIGTPYWMAPE VAAVER	
HH498	WMAPEVFTQCTR	•
HPK1	LSFIGTPYWMAPEVAAVALK	
LOK	DSFIGTPYWMAPEVVMCETMK	KSH1,2,HPK1, SLK
LZK	MSFAGTVAWMAPEVIR	
MAP3K	SMHGTPYWMAPEVINESGYGR	
MST1	NTVIGTPFWMAPEVIQEIGYNCVR	MST2
MST4	NTFVGTPFWMAPEVIQQSAYDSK	
MY03A	NTSVGTPFWMAPEVIACEQQLDTTYDAR	MY03B
MY03B	NTSVGTPFWMAPEVIACEQQYDSSYDAR	MY03A
ZC1/HGK	NTFIGTPYWMAPEVIACDENPDATYDYR	ZC2, ZC3
OSR1	TFVGTPCWMAPEVMEQVR	
PAK1	STMVGTPYWMAPEVVTR	PAK2,3
PAK5	SLVGTPYWMAPEVISR	PAK6
RAF1	WSGSQQVEQPTGSVLWMAPEVIR	•
STLK3	TFVGTPCWMAPE VMEQVR	•
TAO1	ASMASPANSFVGTPYWMAPEVILAMDEGQYDGK	TAO3
TAO2	ASIMAPANSFVGTPYWMAPEVILAMDEGQYDGK	
TESK1	EPLAVVGSPYWMAPEVLR	
ZAK	TTHMSLVGTFPWMAPEVIQSLR	
BL	UE = PET	
RE	D = Commone Epitope	

Figure 20

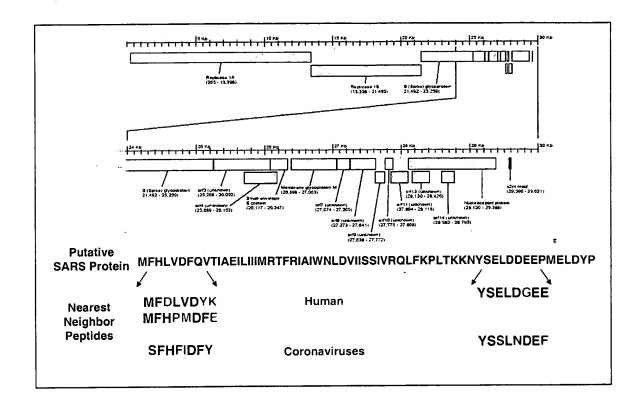


Figure 21

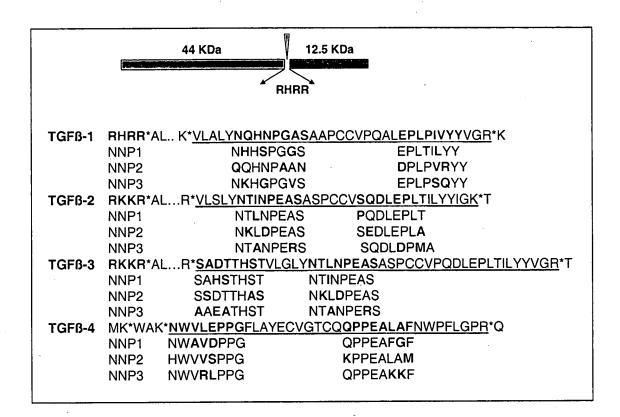


Figure 22

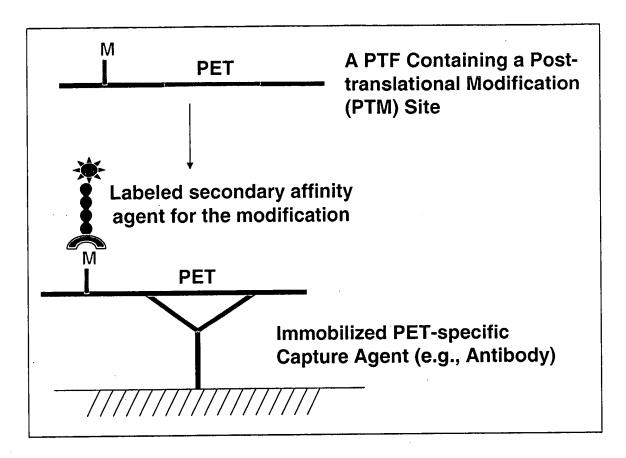


Figure 23

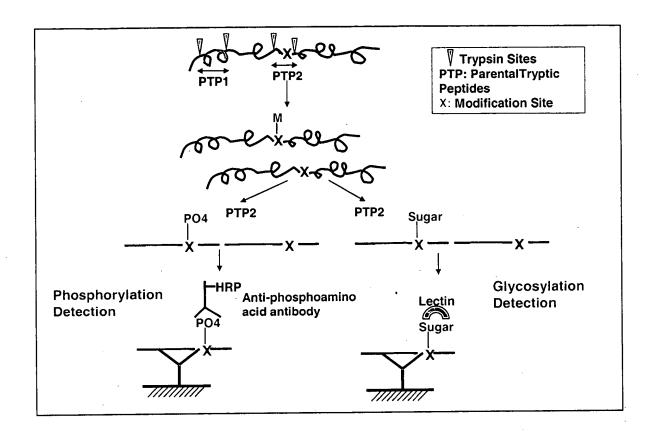


Figure 24

